



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142232

TO: James Schultz
Location: REM-2D18&2C18
Art Unit: 1635
Tuesday, January 25, 2005

Case Serial Number: 09163289

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Schultz,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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142232

From: Schultz, James
Sent: Tuesday, January 11, 2005 11:24 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/163,289

Hello,

I need a standard nucleotide sequence search run against SEQ ID NO:3 in the above entitled application. Please include the interference databases.

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

CRFE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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FEATURES	Location/Qualifiers
Source	1. 164
	/organism="synthetic construct"
	/mol_type="genomic DNA"
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Query Match	60.5%; Score 127.6; DB 6; Length 164;
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Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY	1 AUACTUACCTGGCAGGGGAGAUACCAGUACAGAGUGUGUUUCCACGGCGAGGCTU 60
Db	1 AATCTTACCTGGCAGGGAGATACCATGATCAGAGAGGTGTTTCCACGGCGAGGCTT 60
QY	61 AUCCAUUGGACUCCCGAGUGUGUGACCCCGGCGAUUUUCCCAAUUGUGGAAACUGGACU 120
Db	61 ATCCATTGCACTCCGGATGTGTGTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGACT 120
QY	121 GCAGAAUUGGCGAU 134
Db	121 GCATAATTGTGGT 134
RESULT 4	
HUMUR1A	165 bp snRNA linear PRI 14-JAN-1995
LOCUS	Human U1A small nuclear RNA.
DEFINITION	
ACCESSION	K00788
VERSION	K00788.1 GI:174936
KEYWORDS	U1 small nuclear RNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 165)
TITLE	Brantant,C., Krol,A., Ebel,J.P., Lazar,E., Gallinaro,H., Jacob,M., Sri-Widada,J. and Jeanreut,P.
JOURNAL	Nucleotide sequences of nuclear U1A RNAs from chicken, rat and man
MEDLINE	81053758
PUBMED	6159587
REFERENCE	2 (bases 1 to 63; 76 to 98; 111 to 149)
AUTHORS	Lin,W.L. and Pederson,T.
TITLE	Ribonucleoprotein organization of eukaryotic RNA. XXXI. Structure of the U1 small nuclear ribonucleoprotein
JOURNAL	J. Mol. Biol. 180 (4), 947-960 (1984)
MEDLINE	85134903
PUBMED	6084724
REFERENCE	3 (bases 1 to 165)
AUTHORS	Reveilland,I., Lelay-Taha,M.N., Sri-Widada,J., Brunel,C. and Jeanreut,P.
TITLE	M2+ induces a sharp and reversible transition in U1 and U2 small nuclear ribonucleoprotein configurations
JOURNAL	Mol. Cell. Biol. 4 (9), 1890-1899 (1984)
MEDLINE	85036342
PUBMED	6238232
COMMENT	Original source text: Human Hela cell uRNA.
FEATURES	The trimethylguanosine cap was experimentally determined [1],[2].
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	/mol_type="snRNA"
	/db_xref="taxon:9606"
	/map="1p36.1"
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	/gene="RNU1"
	1. 165
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	/note="U1 small nuclear RNA; G00-119-560"
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/note="pseudouridine (putative) [1] ; putative"
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/note="methyl-adenine"
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Origin      5' end of U1A urRNA.

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Best Local Similarity	73.1% Pred. No. 5.8e-30;
Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY	1 AUACUUAACCCUGGACGAGGAGAUACCAUGAUACGAAAGGUGUUUUCCAGGCGGAGGCU 60
DB	2 ATACTTACCTGGCAGGGGAGATACCATGATCAAGAAAGGTGGTTTCCAGGGCGAGGCTT 61
QY	61 AUCCAUUGGACUCCCGGAGUUGUCUACCCCGUCGAUUUCCCAAAUUGUGGAAACUCGACU 120
DB	62 ATCATTTGCACTCCGGAGTGTCTGACCCCTCGATTTCGCCAAATGTGGAAATCTGACT 121
QY	121 GCAGAUUUGCGCAU 134
DB	122 GCATTAATTTGTGTGT 135
RESULT 5	
LOCUS	AR424957 203 bp DNA linear PAT 18-DEC-2003
SEQUENCE	Sequence 16454 from patent US 6639063.
ACCESSION	AR424957
VERSION	AR424957.1 GI:40180067
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 203)
TITLE	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
JOURNAL	EST's and encoded human proteins
FEATURES	Patent: US 6639063-A 16454 28-Oct-2003;
SOURCE	Location/Qualifiers
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	/mol_type="genomic DNA"
ORIGIN	
Query Match	60.5% Score 127.6; DB 6; Length 203;
Best Local Similarity	73.1% Pred. No. 5.8e-30;
Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY	1 AUACUUAACCCUGGACGAGGAGAUACCAUGAUACGAAAGGUGUUUUCCAGGCGGAGGCU 60
DB	1 ATACTTACCTGGCAGGGGAGATACCATGATCAAGAAAGGTGGTTTCCAGGGCGAGGCTT 60
QY	61 AUCCAUUGGACUCCCGGAGUUGUCUACCCCGUCGAUUUCCCAAAUUGUGGAAACUCGACU 120
DB	61 ATCATTTGCACTCCGGAGTGTCTGACCCCTCGATTTCGCCAAATGTGGAAATCTGACT 120
QY	121 GCAGAUUUGCGCAU 134

Db 121 GCATTAATTGGGT 134

RESULT 6
LOCUS AX985651 203 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 16454 from Patent EP1104808.
ACCESSION AX985651
VERSION AX985651.1 GI:40991791

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Dumas M,Line Edwards,J.B., Jobert,S. and Giordano,J.Y.
ESTs and encoded human proteins
Patent: EP 1104808-A 16454 06-JUN-2001;

JOURNAL Genset (FR)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match	Similarity	60.5%	Score 127.6	DB 6	Length 203
Best Local	Similarity	73.1%	Pred. No. 5.8e-30		
Matches	98	Conservative	32	Mismatches	4
				Indels	0
				Gaps	0
Qy	1	AUACUACCCUGGCGAGGAGAUACCAUGAUCACGAGGUGUGUUUCCGAGGCGAGCGCU	60		
Dh	1	ATATCTTACCTGGCGAGGAGATACCATGATCACGAAAGTGATTTCCAGGGCGAGGCTT	60		
Qy	61	AUCCAUUGGCACTCCCGGAGUGGUCUGACCCCGCCGAAUUUCCCAAUUGUGGAGAAUUCACU	120		
Dh	61	ATCCATTGCACTCCGAGTGTGTGACCCCGCATTTTCCCAATGTGGAGAACTGACT	120		
Qy	121	GCAGAAUUGGCGAU	134		
Dh	121	GCATATTTTGTGGT	134		
RESULT 7	BD120510	203 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD120510	EST and encoded human protein.			
DEFINITION	BD120510	BD120510.1 GI:23215420			
VERSION	JP 2002010789-A/12587				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 203)				
AUTHORS	Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.				
TITLE	EST and encoded human protein				
JOURNAL	Patent: JP 2002010789-A 12587 15-JUN-2002;				
COMMENT	GENSET CORP				
	OS Homo sapiens (human)				
	PN JP 2002010789-A/12587				
	PD 15-JAN-2002				
	PF 07-AUG-2000 JP 2002080989				
	PR 05-AUG-1999 US 60/147499				
	PI JEAN BAPTISTE DUMAS MILNE EDMARDS,SEVELIN JOBERT,JEAN EVE				
	GIORDANO				
	PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC				
	C12N1/21,				
	PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC				
	C12N15/00				
	CC EST and encoded human protein				
	FH Key				
	Location/Qualifiers				

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FEATURES	FT	Location/Qualifiers		
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Query Match		60.5%;	Score 127.6;	DB 6;
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Matches	98;	Conservative	32;	Mismatches 4; Indels 0; Gaps 0;
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QY	61	AUCCAUUGGCAUCCGGAUGUCUGAACCCUCCGCAUUAUCCCAAUUGUGGAAACUCGACU	120	
DB	61	ATCCATTGCACTCCGGAGTGTCTGACCCCTCGATTTCGCCAAATGTGGAAACTCGACT	120	
QY	121	GCAGAUUUGCGCAU	134	
DB	121	GCATTAATTGTGGT	134	
RESULT 8				
LOCUS	AR424959	231 bp	DNA	linear
DEFINITION	Sequence 16456 from patent US 6639063.			PAT 18-DEC-2003
ACCESSION	AR424959			
VERSION	AR424959.1	GI:40180069		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 231)			
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.			
TITLE	Est's and encoded human proteins			
JOURNAL	Patent: US 6639063-A 16456 28-OCT-2003;			
FEATURES	location/Qualifiers			
source	1..231			
ORIGIN	/organism="unknown"			
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DB	1	ATACCTTACCTGGCAGGGAGATACCATGATCAGCAAGGTGGTTTCCAGGGCGAGGCTT	60	
QY	61	AUCCAUUGGCAUCCGGAUGUCUGAACCCUCCGCAUUAUCCCAAUUGUGGAAACUCGACU	120	
DB	61	ATCCATTGCACTCCGGAGTGTCTGACCCCTCGATTTCGCCAAATGTGGAAACTCGACT	120	
QY	121	GCAGAUUUGCGCAU	134	
DB	121	GCATTAATTGTGGT	134	
RESULT 9				
LOCUS	AX985653	231 bp	DNA	linear
DEFINITION	Sequence 16456 from Patent EP104808.			PAT 15-JAN-2004
ACCESSION	AX985653			
VERSION	AX985653.1	GI:40991793		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1
TITLE	Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
JOURNAL	Ests and encoded human proteins
	Patent: EP 1104808-A 16456 06-JUN-2001;
FEATURES	Genset (PR)
source	Location/Qualifiers
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	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
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Best Local Similarity	73.1%; Pred. No. 5.9e-30;
Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
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QY	61 AUCCAUUGGACUCGCGAGUUGUCUGACCCUGCAUUVUCCCAAAUUGUGGAAACUCGACU 120
DB	61 ATCCATTGCACTCCGGAGTGTCTACCCCTCGCATTTCCCAATGTGGAAACTGACT 120
QY	121 GCAGAUUUGCGAU 134
DB	121 GCATATATTGTGGT 134
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LOCUS	BD120512 231 bp DNA linear PAT 18-SEP-2002
DEFINITION	EST and encoded human protein.
ACCESSION	BD120512
VERSION	BD120512.1 GI:23215422
KEYWORDS	JP 2002010789-A/12589.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 231)
TITLE	Edwards, J.B.D.W., Jobert, S. and Giordano, J.E.
JOURNAL	Ests and encoded human protein
	Patent: JP 2002010789-A 12589 15-JAN-2002;
COMMENT	GENSET CORP
OS	Homo sapiens (human)
PN	JP 2002010789-A/12589
PD	15-JAN-2002
PR	07-AUG-2000 JP 20020280969
PR	05-AUG-1999 US 60/147499
PI	JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
	GIORDANO
PC	Cl2N15/09, Cl2N15/09, C07K14/47, C07K16/18, Cl2N1/15, Cl2N1/19, PC
	Cl2N1/21,
PC	Cl2N5/10, Cl2P21/02, Cl2P21/08, Cl2Q1/68, Cl2N15/00, Cl2N5/00, PC
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Best Local Similarity	73.1%; Pred. No. 5.9e-30;
Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
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QY	61 AUCCAUUGGACUCGCGAGUUGUCUGACCCUGCAUUVUCCCAAAUUGUGGAAACUCGACU 120
DB	61 ATCCATTGCACTCCGGAGTGTCTACCCCTCGCATTTCCCAATGTGGAAACTGACT 120
QY	121 GCAGAUUUGCGAU 134
DB	121 GCATATATTGTGGT 134

Db 1 ATACTTACCTGGAGGAGATACATGATCAGAAAGTGTTTCCAGGGGAGGCTT 60
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RESULT 11
HSRNO4
LOCUS HSRNO4 301 bp DNA linear PRI 06-JUL-1989
DEFINITION Human gene possibly encoding UI RNA.
ACCESSION V00587
VERSION V00587.1 GI:36076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 301)
JOURNAL Monstein,H.J., Westin,G., Philipson,L. and Pettersson,U.
MEDLINE EMBO J. 1 (1), 133-137 (1982)
PUBMED 84182447
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AUAUCUACCGGAGGAGAGAUACAUAGCAUAGGAGUUGUCCAGGGGAGGACU 60
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Qy 61 AUCCAUUGCAGCUCGGAUGUGUCUACCCCGGAGAUUUUCCCAAUUGGGAAACUGGACU 120
Db 143 ATCTTACTCTGGAGGGAGATACATGATCAGAAAGTGTTTCCAGGGGAGGCTT 202
Qy 121 GCAGAAUUGGCGGCU 134
Db 203 GCATTAATTTGTGTGT 216

RESULT 12
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LOCUS AR424955 355 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16452 from patent US 6639063.
ACCESSION AR424955
VERSION AR424955.1 GI:40180065
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 355)
TITLE Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
JOURNAL EST's and encoded human proteins
FEATURES Patent: US 6639063-A 16452 28-OCT-2003;
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Best Local Similarity 73.1%; Pred. No. 5.9e-30;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AUAUCUACCGGAGGAGAGAUACAUAGCAUAGGAGUUGUCCAGGGGAGGACU 60
Db 1 ATCTTACTCTGGAGGGAGATACATGATCAGAAAGTGTTTCCAGGGGAGGCTT 60
Qy 61 AUCCAUUGCAGCUCGGAUGUGUCUACCCCGGAGAUUUUCCCAAUUGGGAAACUGGACU 120
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Db 121 GCATTAATTTGTGTGT 134

RESULT 13
AX985649
LOCUS AX985649 355 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 16452 from Patent EP1104808.
ACCESSION AX985649
VERSION AX985649.1 GI:40991789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Homo sapiens
TITLE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Genset (FR)
1
Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
ESTs and encoded human proteins
Patent: EP 1104808-A 16452 06-JUN-2001;
Genset (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 60.5%; Score 127.6; DB 6; Length 355;
Best Local Similarity 73.1%; Pred. No. 5.9e-30;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AUAUCUACCGGAGGAGAGAUACAUAGCAUAGGAGUUGUCCAGGGGAGGACU 60
Db 1 ATCTTACTCTGGAGGGAGATACATGATCAGAAAGTGTTTCCAGGGGAGGCTT 60
Qy 61 AUCCAUUGCAGCUCGGAUGUGUCUACCCCGGAGAUUUUCCCAAUUGGGAAACUGGACU 120
Db 61 ATCTTACTCTGGAGGGAGATACATGATCAGAAAGTGTTTCCAGGGGAGGCTT 120
Qy 121 GCAGAAUUGGCGGCU 134
Db 121 GCATTAATTTGTGTGT 134

RESULT 14
BD120508
LOCUS BD120508 355 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD120508
VERSION BD120508.1 GI:23215418
KEYWORDS JP 2002010789-A/12585.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE EST and encoded human protein

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 14:11:14 : Search time 281 Seconds
(without alignments)
3941.736 Million cell updates/sec

Title: US-09-163-289a-3

Perfect score: 211

Sequence: 1 aaucuuaccuggcagggag.....ucguuucgcuuuccucug 211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205.4	97.3	212	2	AAV32602
2	143.8	68.2	208	12	AD134065
3	127.6	60.5	164	6	ABA92582
4	127.6	60.5	746	4	AAK92184
5	127.6	60.5	746	4	AAK93450
6	127.6	60.5	746	12	AD128611
7	127.6	60.5	746	12	AD129877
8	127.6	60.5	781	4	AAH07536
9	127.6	60.5	1858	4	AAK94493
10	127.6	60.5	1858	12	AD131299
11	127.6	60.5	1912	5	AAK64548
12	127.6	60.5	1914	4	AAK94440
13	127.6	60.5	1914	12	AD131195
14	127.6	60.5	1956	4	AAH14832
15	127.6	60.5	118067	12	AD131110
16	127.6	60.5	118067	12	AD131256
17	126	59.7	165	2	AAK93939
18	126	59.7	165	2	AAK84883
19	122	57.8	122	2	AAK96717
20	121.2	57.4	167	12	ACH84933
21	121.2	57.4	515	12	ACH71233

22	121.2	57.4	607	10	ADD27745	Add27745 pGem3z+U
23	119.4	56.6	825	4	AA195431	Aa195431 Human neu
24	116.8	55.4	164	2	AA089146	Aa089146 RNA molec
25	116.4	53.2	607	10	ADD27746	Add27746 pGem3z+U
26	115.8	54.9	909	5	AAK69273	Aa69273 DNA encod
27	115.8	54.9	909	5	AAK64549	Aa64549 DNA encod
28	115.6	54.8	1343	4	AAK80095	Aa80095 Human imm
29	115.6	54.8	1343	4	AAK80094	Aa80094 Human imm
30	115.6	54.8	1354	4	AAK80093	Aa80093 Human imm
31	115.6	54.8	1354	4	AAK80092	Aa80092 Human imm
32	115.6	54.8	1354	4	AAK80091	Aa80091 Human imm
33	115.6	54.8	1354	4	AAK80090	Aa80090 Human imm
34	115.6	54.8	1470	4	AAK80091	Aa80091 Human imm
35	112.2	53.2	4639	6	AAK39652	Aa39652 Human sma
36	111.6	52.9	365	3	AAK32349	Aa32349 Human sec
37	110	52.1	139	3	AAK87354	Aa87354 Rat hepat
38	109.6	51.9	593	12	ACH68354	Ac168354 Human gen
39	109	51.7	607	10	ADD27763	Add27763 pGem3z+U
40	108	51.2	607	10	ADD27761	Add27761 pGem3z+U
41	106.8	50.6	607	10	ADD27764	Add27764 pGem3z+U
42	106.2	50.3	607	10	ADD27762	Add27762 pGem3z+U
43	104.8	49.7	402	4	AA188559	Aa188559 Human pol
44	103	48.8	107	3	AAK14652	Aa14652 Human sec
45	102.6	48.6	639	12	AD13089	Ad13089 Hypermeth

ALIGNMENTS

RESULT 1	
ID	AAV32602
AAV32602	standard; RNA; 212 BP.
XX	AAV32602;
AC	
XX	
XX	23-SEP-1998 (first entry)
DT	
XX	
XX	Chimeric UI snRNA.
DE	
XX	Fibrillin mRNA; UI snRNA gene; hammerhead ribozyme loop; growth factor;
KW	alzheimer's disease; huntingdon's disease; hereditary parkinsonism;
KM	toxic peptide; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
FH	
FT	Key
FT	Location/Qualifiers
FT	1
FT	/*tag= a
FT	/note= "Optionally mono- or timethyl-guanosine cap"
FT	15. .17
FT	/*tag= b
FT	/note= "Forms double stranded region with bases 120-122"
FT	19. .49
FT	/*tag= c
FT	50. .93
FT	/*tag= d
FT	94. .119
FT	/*tag= e
FT	121. .124
FT	/*tag= f
FT	/note= "Forms double stranded region with bases 14-16"
FT	131. .144
FT	/*tag= g
FT	/note= "Forms double stranded region with bases 17-30 of
FT	the target mRNA molecule (AAV32603)"
FT	145. .166
FT	/*tag= h
FT	/note= "Hammerhead ribozyme loop"
FT	152. .163
FT	/*tag= i
FT	/function= "Catalytic domain"
FT	167. .181
FT	misc_binding

```
FT FT /*tag= j
FT FT /note= "Forms double stranded region with bases 1-15 of
FT FT the target mRNA molecule (AAV2603) "
FT FT stem_loop
FT FT 187..212
FT FT /**tag= k
XX XX
XX XX W09818811-A1.
XX XX
XX XX 07-MAY-1998.
XX XX
XX XX 31-OCT-1997; 97WO-US019849.
XX XX
XX XX 31-OCT-1996; 96US-00742943.
XX XX
XX XX (UWJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX XX
XX XX Dietz HC;
XX XX
XX XX WPI; 1998-272128/24.
XX XX
XX XX Nucleic acid construct expressing antisense nucleic acid - used for
XX XX suppression of gene expression for treating numerous diseases.
XX XX
XX XX Example 1; Fig 1; 43pp; English.
XX XX
XX XX The present sequence represents a chimeric U1 snRNA molecule which
XX XX comprises of a 5' and 3' end unmodified stem loop structure separated by
XX XX the antisense core sequence. The antisense core sequence would itself
XX XX comprise of the first 15 coding nucleotides of the fibrillin mRNA
XX XX followed by the 22 bp hammerhead ribozyme loop which is followed by
XX XX coding nucleotides 17-30 of the fibrillin mRNA. The whole chimeric snRNA
XX XX molecule is an example of a novel nucleic acid construct for suppressing
XX XX expression of a target gene. In the example given, the target gene was
XX XX the fibrillin gene. The antisense core sequence of the chimeric snRNA
XX XX molecule would basepair with the fibrillin mRNA, thus suppressing its
XX XX translation. The invention claims that such nucleic acid constructs can
XX XX be used for suppressing gene expression in vivo, in vitro and ex vivo.
XX XX The constructs are also claimed to be useful for producing non-human
XX XX knock-out animals. Therefore, the construct may be useful for treating
XX XX Alzheimer's disease, Huntington's disease, hereditary Parkinsonism and
XX XX other inherited diseases. They may also be useful for treating enzymatic
XX XX related disorders, and for reducing expression of growth factors, toxic
XX XX peptides, ligands, receptors or other proteins
XX XX
XX XX
XX XX Sequence 212 BP; 45 A; 59 C; 60 G; 0 T; 48 U; 0 Other;
SQ
Query Match 97.3%; Score 205.4; DB 2; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.2e-61;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 UUAACUUGGCGAGGAGAUACCAUGAUGUUGUCCGAGGCGAGGCUUAVCC 64
Db 6 UUAACUUGGCGAGGAGAUACCAUGAUGUUGUCCGAGGCGAGGCUUAVCC 65
QY 65 AUGGACUCCGGAUGUGUCUGACCCCGUGCAUUVUCCCAAUUGUGGAGAAUCUGACUGCAG 124
Db 66 AUGGACUCCGGAUGUGUCUGACCCCGUGCAUUVUCCCAAUUGUGGAGAAUCUGACUGCAG 125
QY 125 AAUUGGCGAUCUCCAGACUUGAUGUCCGUGAGAGCAAAAGCCCUCCAGCAUCUAGU 184
Db 126 AAUUGGCGAUCUCCAGACUUGAUGUCCGUGAGAGCAAAAGCCCUCCAGCAUCUAGU 185
QY 185 GGGGGAACUGGCGUGGCGCUUUCUCCUG 211
Db 186 GGGGGAACUGGCGUGGCGCUUUCUCCUG 212
RESULT 2
AD134065
ID AD134065 standard; RNA; 208 BP.
XX
AC AD134065;
XX
```

```
DT 22-APR-2004 (first entry)
XX
XX N-Smase hammerhead ribozyme.
DE
XX ss; ribozyme; N-Smase mRNA; neutral sphingomyelinase inhibition;
XX apoptosis; atherosclerosis; inflammatory disorder; arthritis;
XX osteoarthritis; Crohn's disease; obesity; diabetes; HIV; liver disorder;
XX cirrhosis; excessive cholesterol; renal failure; central nervous system;
XX CNS disorder; depression; schizophrenia; Alzheimer's disease; hammerhead.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH stem_loop 18..48
XX FT /*tag= a
XX FT stem_loop 49..92
XX FT /*tag= b
XX FT stem_loop 93..118
XX FT /*tag= c
XX FT stem_loop 151..162
XX FT /*tag= d
XX FT stem_loop 186..207
XX FT /*tag= e
XX
XX US2004006039-A1.
XX
XX 08-JAN-2004.
XX
XX 27-MAY-2003; 2003US-00446519.
XX
XX 23-OCT-2001; 2001US-0342631P.
XX 23-OCT-2002; 2002US-00279215.
XX
XX (CHAT/) CHATTERJEE S B.
XX
XX Chatterjee SB;
XX
XX WPI; 2004-081746/08.
XX
XX New nucleic acid molecule comprising a ribozyme that is specific for N-
XX Sase mRNA, useful for treating inflammatory disorders such as arthritis,
XX osteoarthritis, Crohn's disease, obesity, diabetes, HIV, or liver
XX disorders.
XX
XX Claim 3; SEQ ID NO 1; 25pp; English.
XX
XX
XX The present sequence represents a nucleic acid molecule comprising a
XX ribozyme that is specific for N-Smase mRNA. The nucleic acid molecule is
XX useful for inhibiting the activity of neutral sphingomyelinase and for
XX reducing apoptosis and atherosclerosis. The molecule and methods are
XX useful for treating inflammatory disorders such as arthritis,
XX osteoarthritis, Crohn's disease, obesity, diabetes, HIV, liver disorders
XX (e.g. cirrhosis), excessive cholesterol levels, renal failure, or central
XX nervous system (CNS) disorders such as depression, schizophrenia or
XX Alzheimer's disease. The present sequence represents the N-Smase
XX hammerhead ribozyme.
XX
XX Sequence 208 BP; 48 A; 54 C; 56 G; 0 T; 50 U; 0 Other;
SQ
Query Match 68.2%; Score 143.8; DB 12; Length 208;
Best Local Similarity 85.6%; Pred. No. 4.7e-40;
Matches 172; Conservative 0; Mismatches 27; Indels 2; Gaps 1;
QY 8 CUGGCGAGGAGAGAUACCAUGAUGUUGUCCGAGGCGAGGCUUAVCC 67
Db 9 CUGGCGAGGAGAGAUACCAUGAUGUUGUCCGAGGCGAGGCUUAVCC 68
QY 68 GCACUCCGGAUGUGUCUGACCCCGUGCAUUVUCCCAAUUGUGGAGAAUCUGACUGCAGAU 127
Db 69 GGCACCGGAUGUGUCUGACCCCGUGCAUUVUCCCAAUUGUGGAGAAUCUGACUGCAGAU 128
QY 128 UGGCAUUCUCCAGACUUGAUGUCCGUGAGAGCAAAAGCCCUCCAGCAUCUAGUGGG 187
```

Db 129 AUGUCAUAAUUGCCUGAGUCGUGAGAGAAACCUUCUACAUAAAAAGUGG 188
QY 188 GGAUCUGGUGCGGCUUCCC 208
Db 189 G--CUGCGUUGCGGCUUCCCC 207

RESULT 3
ABA92582

ID ABA92582 standard; DNA; 164 BP.

XX ABA92582;

DT 21-MAR-2002 (first entry)

DE UIDNA amplification product SEQ ID NO:3.

XX Anti-ENA antibody; extractable nuclear antigen; collagen disease;
KM systemic erythematode; intracellular non-histone soluble protein;
KW skin toughening; ds.

OS Synthetic.

PN WO200190756-A1.

PD 29-NOV-2001.

PF 21-MAY-2001; 2001WO-0P004251.

PR 26-MAY-2000; 2000JP-00157410.

PA (MED-) MEDICAL & BIOLOGICAL LAB CO LTD.

PI Murakami A, Kojima K;

PI WPI; 2002-089938/12.

XX Assaying anti-extractable nuclear antigen (ENA) antibody based on
PT reaction of antigen complex with specimen, applicable in diagnosis of
PT collagen diseases e.g. systemic erythematodes and skin toughening.

PS Example 1; Page 53; 59pp; Japanese.

XX The present invention describes assaying anti-extractable nuclear antigen
CC (ENA) antibody recognising an antigen containing a first RNA and a first
CC intracellular non-histone soluble protein, comprising forming a complex
CC between a second RNA and a first protein molecule, reacting such complex
CC with a specimen, and detecting the reaction product. The method is
CC applicable in the diagnosis of collagen diseases e.g. systemic
CC erythematodes and skin toughening. The method is convenient and highly
CC sensitive, which is comparable with the conventional DID method, with
CC reagents easy to handle and store. The present sequence represents a
CC UIDNA nucleotide sequence, which is used in an example from the present
CC invention

SQ Sequence 164 BP; 32 A; 42 C; 47 G; 43 T; 0 U; 0 Other;

Query Match 60.5%; Score 127.6; DB 6; Length 164;

Best Local Similarity 73.1%; Pred. No. 2.1e-34;

Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCGGAGGAGAGAUACAUAGUACGAAAGUGUUTUCCAGGCGGAGGCU 60

Db 1 AUAUCUACCGGAGGAGAGATACATGATCAGAAAGTGTTTCCAGGCGGAGGCTT 60

QY 61 AUCGAUUGGAGUUGUGUGUGAGUUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 120

Db 61 ATTCATTGCACTCGGATGCTGACCCCTCGCATTTCCCAATGTGGAAACTGACT 120

QY 121 GCAGAAUUGGCGAU 134

Db 121 GCATAATTGTGTGT 134

RESULT 4
ID AAK92184 standard; cDNA; 746 BP.

XX AAK92184;

DT 06-NOV-2001 (first entry)

DE Human cDNA 5'-end sequence, SEQ ID NO: 644.

KM Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

PN EP130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

PA (HELT-) HELIX RES INSTR.

PI Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y, H;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

PI WPI; 2001-524255/58.

PS Claim 2; SEQ ID NO 644; 1380BP + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is the nucleotide sequence of the 5'-end of
CC a cDNA provided in the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in CD-
CC ROM format directly from EPO

SQ Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;

Query Match 60.5%; Score 127.6; DB 4; Length 746;

Best Local Similarity 73.1%; Pred. No. 3.6e-34;

Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCGGAGGAGAGAUACAUAGUACGAAAGUGUUTUCCAGGCGGAGGCU 60

Db 1 AUAUCUACCGGAGGAGAGATACATGATCAGAAAGTGTTTCCAGGCGGAGGCTT 60

QY 61 AUCGAUUGGAGUUGUGUGUGAGUUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 120

Db 61 ATTCATTGCACTCGGATGCTGACCCCTCGCATTTCCCAATGTGGAAACTGACT 120

QY 121 GCAGAAUUGGCGAU 134

Db 121 GCATAATTGTGTGT 134

RESULT 5

ID AAK93450 standard; cDNA; 746 BP.

XX AAK93450

```

AC      AAK93450;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human cDNA clone representative sequence, SEQ ID NO: 1910.
XX
KW      Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS      Homo sapiens.
XX
PN      EP1130094-A2.
XX
PD      05-SEP-2001.
XX
PF      07-UTL-2000; 2000EP-00114089.
XX
PR      08-JUL-1999; 99JP-00194486.
XX
PR      11-JAN-2000; 2000JP-00118774.
XX
PR      02-MAY-2000; 2000JP-00183765.
XX
PA      (HELI-) HELIX RES INST.
XX
PI      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI      Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR      WPI, 2001-524255/58.
XX
XX
XX      830 Primers useful for synthesizing full length cDNA clones and their use
XX      in genetic manipulation.
XX
PS      Example 11; SEQ ID NO 1910; 1380bp + Sequence Listing; English.
XX
XX
XX      The invention relates to primers for synthesizing full length cDNA
XX      clones. 830 cDNA molecules encoding a human protein have been isolated
XX      and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX      been determined. Primers for synthesizing the full length cDNA are useful
XX      for clarifying the function of the protein encoded by the cDNA. The full
XX      length clones were obtained by construction of full length enriched cDNA
XX      libraries that were synthesised by the oligo-capping method. The primers
XX      enable the production of the full length cDNA easily without any special
XX      methods. The present sequence was used as the representative sequence
XX      from a human clone which was used in homology searches to identify the
XX      clone. Note: The sequence data for this patent did not form part of the
XX      printed specification, but was obtained in CD-ROM format directly from
XX      EPO
XX
SQ      Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;
XX
XX
XX      Query Match      60.5%; Score 127.6; DB 4; Length 746;
XX      Best Local Similarity 73.1%; Pred. No. 3, 6e-34;
XX      Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0
XX
OY      1 ATACUACCCUGGCGAGGGGAGAUACCAUGAUACAAGAGUGGUUUUCCCAAGGGGAGAGCUU 60
DB      1 ATACTTACTCTGGCAGGGGAGATPACCATGATCACGAAGGTTTCCACGGGGGAGAGCTT 60
OY      61 AUCCAUUGCACCUCGAGUUGUCGACCCCGUGCGAUUUCCCAAUUGGGAAACUCGACU 120
DB      61 ATCCATGTGACATCCGGATGTGCTGACCCCTGTGCATTTCCCAATGTGGAAACTGACT 120
OY      121 GCAGAUUUGCGAU 134
DB      121 GCATATTTGTGTGT 134
XX
XX
XX      RESULT 6
XX      ADL28611
XX      ID      ADL28611 standard; cDNA; 746 BP.
XX
XX      AC      ADL28611;
XX
XX      DT      20-MAY-2004 (first entry)
XX

```

XX	5'	end of a human cDNA molecule	Seqid 644.	
XX	human;	medicine; signal transduction; glycoprotein; transcription;		
XX	oligo-capping method; ss.			
XX	Homo sapiens.			
XX	EP1396543-A2.			
XX	10-MAR-2004.			
XX	07-JUL-2000; 2003EP-00025638.			
XX	08-JUL-1999; 98JP-00194486.			
PR	11-JAN-2000; 2000JP-00118774.			
PR	02-MAY-2000; 2000JP-00183865.			
PR	07-JUL-2000; 2000EP-00114089.			
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.			
XX	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,			
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;			
XX	WPI; 2004-204755/20.			
DR	New oligonucleotide primers (830 cDNAs) useful for synthesizing full			
PT	length human cDNAs.			
PS	Disclosure; SEQ ID NO 644; 1340pp; English.			
XX	This invention relates to a novel primers useful for synthesizing full			
CC	length cDNA molecules that encode human proteins. Specifically, it refers			
CC	to secretory or membrane proteins that are potential therapeutic agents/			
CC	target molecules in the field of medicine, and in particular genes			
CC	encoding proteins that are associated with signal transduction,			
CC	glycoproteins and transcription. The present invention describes a method			
CC	for efficiently cloning a full length human cDNA from both the 5' and 3'			
CC	ends using the oligo-capping method. This polynucleotide sequence is the			
CC	5' end of a full length human cDNA sequence of the invention.			
XX	Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;			
XX	Query Match 60.5%; Score 127.6; DB 12; Length 746;			
XX	Best Local Similarity 73.1%; Pred. No. 3.6e-34;			
XX	Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;			
QY	1 AUAACUACCCUGGAGGAGGAGUACCAUGAUUACGAGGAGGAGGAGGU 60			
DB	1 ATACTTACTCTGGCAGGGAGGAGTATACCAATGATGATTTTCCAGGCGAGGCTT 60			
QY	61 AUCCAUUGGACUCCGGAUGUGUCUGACCCUGGCGAUUUCGCCAUAUUGGAGAAACUCCAU 120			
DB	61 ATCATTTGCACTCCGGAATGTCTGACCCCTGCGATTTCCCAAAATGTGGGAAACTCGACT 120			
QY	121 GCAGAUUUGGCGAU 134			
DB	121 GCATTAATTTGTGT 134			
XX	RESULT 7			
XX	ADL29877			
XX	ID ADL29877 standard; cDNA; 746 BP.			
XX	ADL29877;			
XX	20-MAY-2004 (first entry)			
XX	5' end of a representative human cDNA cluster			
XX	Seqid 1910.			
XX	human; medicine; signal transduction; glycoprotein; transcription;			
XX	oligo-capping method; ss.			
XX	Homo sapiens.			

XX Homo sapiens.
 OS
 XX EPI130094-A2.
 PN
 XX
 PD
 XX 05-SEP-2001.
 PF
 XX 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR P-PSDB; AAM93561.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS
 XX Claim 8; SEQ ID NO 3332; 1380bp + Sequence listing; English.
 CC
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in CD-ROM format directly
 CC from BPO
 CC
 SQ Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
 Query Match 60.5%; Score 127.6; DB 4; Length 1858;
 Best Local Similarity 73.1%; Pred. No. 5.1e-34;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AUAUCCUACCGGAGGAGAGUACCAUAGUACAGAGGUGUUNUCCAGGCGAGGCUU 60
 Db 1 AUAUCCUACCGGAGGAGAGUACCAUAGUACAGAGGUGUUNUCCAGGCGAGGCUU 60
 QY 61 AUCGCAUUGCAGUCCGAGUGUGUGUACCCGUGGAGUUNUCCCAAUUGUGGAAACUGGACU 120
 Db 61 ATCCATTGCACTCCGAGATGTGCTGACCCCTGCGATTTCCTCAATGTGGAAACTGCACT 120
 QY 121 GCAGAAUUGCGGAGU 134
 Db 121 GCATAATTGTGTGT 134
 RESULT 10
 ADL31299
 ID ADL31299 standard; cDNA, 1858 BP.
 AC ADL31299;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX
 XX Full length human cDNA clone SegID 3332.
 DE
 XX human; medicine; signal transduction; glycoprotein; transcription;
 KM oligo-capping method; ss; gene.
 XX
 OS Homo sapiens.
 XX

PN EPI1396543-A2.
 XX
 XX 10-MAR-2004.
 PD
 XX
 XX 07-JUL-2000; 2003EP-00025638.
 PF
 XX 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2004-204755/20.
 DR P-PSDB; ADL31300.
 XX
 PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 PS
 XX Example 1; SEQ ID NO 3332; 1340bp; English.
 CC
 CC This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polynucleotide sequence is a
 CC full length human cDNA clone of the invention.
 CC
 SQ Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
 Query Match 60.5%; Score 127.6; DB 12; Length 1858;
 Best Local Similarity 73.1%; Pred. No. 5.1e-34;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AUAUCCUACCGGAGGAGAGUACCAUAGUACAGAGGUGUUNUCCAGGCGAGGCUU 60
 Db 1 AUAUCCUACCGGAGGAGAGUACCAUAGUACAGAGGUGUUNUCCAGGCGAGGCUU 60
 QY 61 AUCGCAUUGCAGUCCGAGUGUGUGUACCCGUGGAGUUNUCCCAAUUGUGGAAACUGGACU 120
 Db 61 ATCCATTGCACTCCGAGATGTGCTGACCCCTGCGATTTCCTCAATGTGGAAACTGCACT 120
 QY 121 GCAGAAUUGCGGAGU 134
 Db 121 GCATAATTGTGTGT 134
 RESULT 11
 AAS64548/c
 ID AAS64548 standard; cDNA, 1912 BP.
 AC AAS64548;
 XX
 XX 13-FEB-2002 (first entry)
 DT
 XX
 XX DNA encoding novel human diagnostic protein #352.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US008631.

PR	31-MAR-2000;	2000US-00540217.
PR	23-AUG-2000;	2000US-00649167.
PA	(HYSE-) HYSEQ INC.	
PI	Drmnac RT, Liu C, Tang YT;	
XX	WPI, 2001-639362/73.	
DR	P-PSDB; AEG00361.	
XX		
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	biodiversity.	
XX		
PS	Claim 1; SEQ ID NO 352; 103bp; English.	
XX		
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
CC	and in recombinant production of (II). The polynucleotides are also used	
CC	in diagnostics as expressed sequence tags for identifying expressed	
CC	genes. (I) is useful in gene therapy techniques to restore normal	
CC	activity of (II) or to treat disease states involving (II). (II) is	
CC	useful for generating antibodies against it, detecting or quantitating a	
CC	polypeptide in tissue, as molecular weight markers and as a food	
CC	supplement. (II) and its binding partners are useful in medical imaging	
CC	of sites expressing (II). (I) and (II) are useful for treating disorders	
CC	involving aberrant protein expression or biological activity. The	
CC	polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic	
CC	coding sequences of the invention. Note: The sequence data for this	
CC	parent did not appear in the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SO	Sequence 1912 BP; 520 A; 521 C; 547 G; 321 T; 0 U; 3 Other;	
Query Match	60.5%; Score 127.6; DB 5; Length 1912;	
Best Local Similarity	73.1%; Pred. No. 5,2e-34;	
Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0.	
QY	1 AUAUCCUACCCUGGACAGGGAGGAUACCAUAGUACGAAAGUGGUUUCCAGAGGCGAGGCU 60	
DB	146 AUAUCCUACCCUGGACAGGGAGGAUACCAUAGUACGAAAGUGGUUUCCAGAGGCGAGGCU 87	
QY	61 AUAUCCUACCCUGGACAGGGAGGAUACCAUAGUACGAAAGUGGUUUCCAGAGGCGAGGCU 120	
DB	86 AUAUCCUACCCUGGACAGGGAGGAUACCAUAGUACGAAAGUGGUUUCCAGAGGCGAGGCU 27	
QY	121 GCAGAAUUGGCGAU 134	
DB	26 GCATTAATTTGTGCT 13	
RESULT 12		
ID	AAK94440 standard; cDNA; 1914 BP.	
XX	AAK94440;	
AC		
XX	07-NOV-2001 (first entry)	
DE	Human cDNA, SEQ ID NO: 3228.	
XX		
KW	Human; full length cDNA; cDNA synthesis; oligo-capping; 68.	
XX		
OS	Homo sapiens.	
XX		

XX	FN	EP1130094-A2.
XX	PD	
XX	PD	05-SEP-2001.
XX	PF	07-JUL-2000; 2000EP-00114089.
XX	PR	08-JUL-1999; 99JP-00194486.
XX	PR	11-JAN-2000; 2000JP-00118774.
XX	PR	02-MAY-2000; 2000JP-00183765.
XX	PA	(HELI-) HELIX RES INST.
XX	PI	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX	PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX	DR	WI; 2001-524255/58.
XX	DR	P-PSDB; AAM93510.
XX	PT	830 Primers useful for synthesizing full length cDNA clones and their use
XX	PT	in genetic manipulation.
XX	PS	Disclosure; SEQ ID NO 3228; 1380bp + Sequence Listing; English.
XX	CC	The invention relates to primers for synthesizing full length cDNA
XX	CC	clones. 830 cDNA molecules encoding a human protein have been isolated
XX	CC	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX	CC	been determined. Primers for synthesizing the full length cDNA are useful
XX	CC	for clarifying the function of the protein encoded by the cDNA. The full
XX	CC	length clones were obtained by construction of full length enriched cDNA
XX	CC	libraries that were synthesized by the oligo-capping method. The primers
XX	CC	enable the production of the full length cDNA easily without any special
XX	CC	methods. The present sequence is a human cDNA provided in the
XX	CC	specification. Note: The sequence data for this patent did not form part
XX	CC	of the printed specification, but was obtained in CD-ROM format directly
XX	CC	from EPO
XX	SQ	Sequence 1914 BP; 554 A; 501 C; 400 G; 459 T; 0 U; 0 Other;
QY		Query Match 60.5%; Score 127.6; DB 4; Length 1914;
QY		Best Local Similarity 73.1%; Pred. No. 5.2e-34;
QY		Matches 98; Conservative % 32; Mismatches 4; Indels 0; Gaps 0;
DB		1 AUAUUCUACCCUGGAGGAGAUACCAUGAUCAGAAUGUGUUUUCCAGGGCAGAGCUU 60
DB		3 ATACTTACCTGGGAGGAGGAGATACCAATGATCACAAGAGTGATTTTCCAGGGCAGAGCTT 62
QY		61 AUCCAUUGGACUCCGGAUGUGUGUACCCUGGCAUUVUCCCAAAUUGUGGAAACUCGACAU 120
DB		63 ATCCATTGACACTCCGGAATGCTCTACCCCTGCGATTTCCTCAATGTGGGAAATCGACT 122
QY		121 GCAGAUUUGGCGAU 134
DB		123 GCATTAATTTGTGTGT 136
RESULT 13		
ADL31195		
ID		ADJ31195 standard; cDNA; 1914 BP.
XX		
AC		ADJ31195;
XX		
DT		20-MAY-2004 (first entry)
XX		
DE		Full length human cDNA clone segid 3228.
XX		
KM		human; medicine; signal transduction; glycoprotein; transcription;
XX		oligo-capping method; ss; gene.
XX		
OS		Homo sapiens.
XX		
XX		EP1396543-A2.
XX		
DD		10-MAR-2004.

PR	02-MAY-2000; 2000JP-00183767.
XX	09-JUN-2000; 2000JP-00241899.
PA	(HELI-) HELIX RES INST.
PI	Ota T., Isogai T., Nishikawa T., Hayashi K., Saito K., Yamamoto J,
PT	Ishii S., Sugiyama T., Wakamatsu A., Nagai K., Otsuki T;
DR	WPI, 2001-318749/34.
XX	
PS	Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT	length cDNAs defined in the specification, and for the detection and/or
PT	diagnosis of the abnormality of the proteins encoded by the full-length
PT	cDNAs.
PS	
XX	Claim 8; SEQ ID NO 12648; 2537bp + Sequence Listing; English.
XX	
CC	The present invention describes primer sets for synthesizing 5602 full-
CC	length cDNAs defined in the specification. Where a primer set comprises:
CC	(a) an oligo-dT primer and an oligonucleotide complementary to the
CC	complementary strand of a polynucleotide which comprises one of the 5602
CC	nucleotide sequences defined in the specification, where the
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC	of an oligonucleotide comprising a sequence complementary to the
CC	complementary strand of a polynucleotide which comprises a 5'-end
CC	sequence and an oligonucleotide comprising a sequence complementary to a
CC	polynucleotide which comprises a 3'-end sequence, where the
CC	oligonucleotide comprises at least 15 nucleotides and the combination of
CC	the 5'-end sequence/3'-end sequence is selected from those defined in the
CC	specification. The primer sets can be used in antisense therapy and in
CC	gene therapy. The primers are useful for synthesizing polynucleotides,
CC	particularly full-length cDNAs. The primers are also useful for the
CC	detection and/or diagnosis of the abnormality of the proteins encoded by
CC	the full-length cDNAs. The primers allow obtaining of the full-length
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC	represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC	oligonucleotides, all of which are used in the exemplification of the
CC	present invention
XX	
SQ	Sequence 1956 BP; 377 A; 632 C; 547 G; 400 T; 0 U; 0 Other;
	Query Match 60.5%; Score 127.6; DB 4; Length 1956;
	Best Local Similarity 73.1%; Pred. No. 5.2e-34;
	Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0
QY	1 AUAUCUACUGGAGCGGGAGAUAUCCAUCAUACGAAGUGGUUUUCCAGGCCGAGGCTU 60
DB	1 ATACTTACTCTGCGAGGGGAGATACCATTGATCAGCAAGAGGTGGTTTCCAGGGCCGAGGCTT 60
QY	61 AUUCAUUGCAUCUCGGAGUGUCUGACCCCUCCGUAUUVUCCCCAAUAGUGUGAAACUCGACU 120
DB	61 ATCATTCGCAATCCGCGAAGTGCTCTAACCCCTCGATTTCGCCAAATGTGGAAACTGCAT 120
QY	121 GCAGAAUUGCGCAU 134
DB	121 GCATAATTGTGGT 134
RESULT 15	
ADFL1110	
ID	ADFL1110 standard; DNA; 118067 BP.
XX	
AC	ADFL1110;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Hypermethylation site in human breast cancer CpG island locus HBC-37.
XX	
DNA	DNA methylation; CpG dinucleotide rich region;
KM	differential methylation hybridisation; DMH; CpG island; screening array;
KM	breast cancer; prostate cancer; colon cancer; lung cancer; liver cancer;
KM	ovarian cancer; human hypomethylated CpG islands

```

XX OS Homo sapiens.
XX PN US2003129602-A1.
XX PD 10-JUL-2003.
XX PF 21-FEB-2002; 2002US-00081327.
XX PR 05-FEB-1999; 99US-0118760P.
XX PR 18-FEB-1999; 99US-0120592P.
XX PR 04-FEB-2000; 2000US-00497855.
XX PA (HUAN/) HUANG T H.
XX PI Huang TH.
XX DR WPI; 2004-031298/03.
XX PT Differential methylation hybridization assay for detecting
XX PT hypermethylation of CpG dinucleotide rich regions in genomic DNA is
XX PT useful to diagnose and monitor breast, prostate, colon, lung, liver and
XX PT ovarian cancer.
XX PS Claim 17; SEQ ID NO 32; 32pp; English.
XX CC The present invention relates to a method of detecting DNA methylation of
XX CC a CpG dinucleotide rich region of a nucleic acid. The method comprises
XX CC hybridization by differential methylation hybridization (DMH) in which
XX CC the nucleic acid is digested into fragments in which CpG islands are
XX CC preserved, attaching the fragments to linker primers, digesting the
XX CC linker primer products to digest unmethylated CpG sequences, amplifying
XX CC and labelling the remaining linker primer products and detecting labelled
XX CC amplicons. Also disclosed is a screening array comprising nucleic acid
XX CC fragments fixed to a solid support where each fragment is a CpG
XX CC dinucleotide rich fragment comprising at least 200 nucleotides of which
XX CC at least 50% are guanine and cytosine. Nucleic acid probes prepared from
XX CC a cell sample are used to screen CpG dinucleotide rich fragments fixed
XX CC onto a screening array. The invention is useful to diagnose and monitor
XX CC prognosis of a disease associated with aberrant DNA methylation,
XX CC particularly breast, prostate, colon, lung, liver or ovarian cancer,
XX CC especially breast cancer. The present sequence represents the site of
XX CC hypermethylation in human breast cancer at a CpG island locus (HBC,
XX CC hypermethylation in breast cancer).
XX SQ Sequence 118067 BP; 28717 A; 29403 C; 28733 G; 31214 T; 0 U; 0 Other;

Query Match          60.5%; Score 127.6; DB 12; Length 118067;
Best Local Similarity 73.1%; Pred. No. 2.4e-33;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAACUACCGGCGAGGAGAUACAUGAUCAGAAAGUGUUUCCAGGCGAGACU 60
DB 59420 ATACTTACTCGGAGGAGATGATCAATGATCAAGAAAGTGTTCCTCCAGGCGAGGCTT 59479
QY 61 AUCCAUUGCAUCCGCGAUGUGUCUGACCCUGCGAUUCCCCAAAUUGGGAAACUCGACU 120
DB 59480 ATCCATTGCACTCCGATGTGTGACCCCTGCGATTTCCTCCAAATGTGGGAAACTCGACT 59539
QY 121 GCAGAAUUGGCGAU 134
DB 59540 GCATTAATTGTGTGT 59553

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Job time : 288 secs

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OM nucleic - nucleic search, using SW model

Run on: January 19, 2005, 17:04:49 ; Search time 73 Seconds
(without alignments)
2054.472 Million cell updates/sec

Title: US-09-163-289A-3

Perfect score: 211
Sequence: 1 auaacucagcgagcgaggggag.....ugcguucgcgcuuuuccug 211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	160.8	76.2	215	US-08-724-354D-26 Sequence 26, Appl
2	160.8	76.2	215	US-09-270-984A-26 Sequence 26, Appl
3	127.6	60.5	203	US-09-621-976-16454 Sequence 16454, A
4	127.6	60.5	231	US-09-621-976-16456 Sequence 16456, A
5	127.6	60.5	355	US-09-621-976-16452 Sequence 16452, A
6	127.6	60.5	118067	US-09-497-855A-32 Sequence 32, Appl
7	127.2	60.3	204	US-09-621-976-16458 Sequence 16458, A
8	126	59.7	189	US-09-621-976-16457 Sequence 16457, A
9	126	59.7	207	US-09-621-976-16455 Sequence 16455, A
10	123.2	58.4	175	US-09-621-976-16453 Sequence 16453, A
11	116.8	55.4	164	US-08-704-170-75 Sequence 75, Appl
12	116.8	55.4	164	PCT-US94-02631-75 Sequence 75, Appl
13	111.6	52.9	365	US-09-513-999C-36424 Sequence 36424, A
14	103.2	48.9	157	US-09-621-976-10271 Sequence 10271, A
15	103	48.8	107	US-09-513-999C-18727 Sequence 18727, A
16	102.6	48.6	639	US-09-497-855A-11 Sequence 11, Appl
17	98.6	46.7	5227	US-09-919-172-79 Sequence 79, Appl
18	98.6	46.7	5228	US-09-919-039-216 Sequence 216, Appl
19	98.2	46.5	1121	US-09-919-172-88 Sequence 88, Appl
20	98.2	46.5	1121	US-09-976-594-848 Sequence 848, Appl
21	95	45.0	179	US-08-781-6208-2 Sequence 2, Appl
22	95	45.0	435	US-08-781-6208-3 Sequence 3, Appl
23	91.8	43.5	434	US-08-781-6208-22 Sequence 22, Appl
24	67.4	31.9	3001	US-09-539-333D-171 Sequence 171, Appl
25	61.8	29.3	133	US-09-513-999C-13542 Sequence 13542, A
26	55	26.1	55	US-08-742-943-1 Sequence 1, Appl
27	55	26.1	55	US-08-742-943-2 Sequence 2, Appl

28	54.4	25.8	826	US-09-919-172-99 Sequence 99, Appl
29	54.4	25.8	826	US-09-976-594-811 Sequence 811, Appl
30	36.8	17.4	148	US-09-513-999C-10581 Sequence 10581, A
31	31.6	15.0	83	US-08-862-337-2 Sequence 2, Appl
32	31	14.7	31	US-08-371-986-16 Sequence 16, Appl
33	30.8	14.6	40	US-08-324-362-4 Sequence 4, Appl
34	30.8	14.6	40	US-08-324-362-5 Sequence 5, Appl
35	30.8	14.6	70	US-09-276-533A-3 Sequence 3, Appl
36	30.8	14.6	70	US-09-276-533A-4 Sequence 4, Appl
37	30.8	14.6	70	US-10-158-735-3 Sequence 3, Appl
38	30.8	14.6	70	US-10-158-735-4 Sequence 4, Appl
39	30.6	14.5	1100	US-09-918-686-18 Sequence 18, Appl
40	30.6	14.5	51719	US-09-918-686-2 Sequence 2, Appl
41	30.6	14.5	92139	US-09-918-686-1 Sequence 1, Appl
42	30.2	14.3	92	US-08-464-073-26 Sequence 26, Appl
43	30.2	14.3	92	US-08-428-252-26 Sequence 26, Appl
44	30	14.2	2508	US-09-489-039A-1569 Sequence 1569, Appl
45	29.8	14.1	47	US-08-695-191-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-724-354D-26
Sequence 26, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic RNA
US-08-724-354D-26
Query Match 76.2%; Score 160.8; DB 2; Length 215;
Best Local Similarity 90.7%; Pred. No. 46-49; 17; Indels 3; Gaps 2;
Matches 194; Conservative 0; Mismatches 17; Indels 3; Gaps 2;
QY 1 AUAUACUACUGGAGGAGGAGUACCAUGAUCGAGAGUGUGUUUCCAGGCGGAGGCUU 60
DB 2 AUAUACUACUGGAGGAGGAGUACCAUGAUCGAGAGUGUGUUUCCAGGCGGAGGCUU 61

QY	61	AUCCAUUGGCACTUCGCGAUGUGCUAGACCCCTUGCGAUAUUCCTCAAAUGUGGGAACUUGCACTU	120
Db	62	AUCCAUUGGCACTUCGCGAUGUGCUAGACCCCTUGCGAUAUUCCTCAAAUGUGGGAACUUGCACTU	121
QY	121	GCAGAATUGGCG - AUUUCGACGACCTUGAUAUGUCCUGAGAGACGAAACGCCCTUCGAC--GC	177
Db	122	GCAGAATUGUGUAGGACCTCCACGCTGAUAGUCCUGAGAGACGAAACGCCCTUCGAC--GC	181
QY	178	AUUCAGUGGGGGGACUUGCGAUUUGCGCCTUUCGCCU	211
Db	182	GCUCAGUGGGGGACUUGCGAUUUGCGCCTUUCGCCU	215

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RESULT 2
US-09-270-984A-26
; Sequence 26, Application US/09270984A
; Patent No. 6048965
;
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
NUMBER OF INVENTION: NONSENSE-MEDIATED RNA DECAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,984A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,354
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic RNA
IS-09-270-984A-26

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Query Match	76.2%:	Score 160.8:	DB 3:	Length 215:
Best Local Similarity	90.7%:	Pred. No. 4e-49:		
Matches 194:	Conservative 0:	Mismatches 17:	Indels 3:	Gaps 2:
QY	1	AUA	CUVUA	CUUGGCGAGGAGAUACCAUUAUACGAAAGUGUGUUUCCAGGGCCGAGGCU 60
Db	2	AUA	CUVUA	CUUGGCGAGGAGAUACCAUUAUACGAAAGUGUGUUUCCAGGGCCGAGGCU 61
QY	61	AUCCA	UUGGCA	CUCCGAGUGUCUGAACCCUCGCUUUAUCCCAAAUGUGGAAAUCUGACU 120
Db	62	AUCCA	UUGGCA	CUCCGAGUGUCUGAACCCUCGCUUUAUCCCAAAUGUGGAAAUCUGACU 121
QY	121	GCA	GAUUGGGG	-AUCUUCACAGACUAGUAGAUCCGUGAGAGCAAAAGCCCTCGAC--GC 177
Db	122	GCA	GAUUGGGG	-AUCUUCACAGACUAGUAGAUCCGUGAGAGCAAAAGCCCTCGAC--GC 181

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Oy      178 AUTCAGUGGGGGA CUGCGUUCGGCGUUTC CCCTG 211
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Db      182 GGCUAUGGGGGA CUGCGUUCGGCGUUTC CCCTG 215

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RESULT 3
US-09-621-976-16454
, Sequence 16454, Application US/09621976
, Patent No. 6639063
, GENERAL INFORMATION:
, APPLICANT: Dumas Milne Edwards, J.B.
, APPLICANT: Jobert, S.
, APPLICANT: Giordano, J.Y.
, TITLE OF INVENTION: Esters and Encoded Human Proteins
, FILE REFERENCE: GENSET, 054PR2
, CURRENT APPLICATION NUMBER: US/09/621,976
, CURRENT FILING DATE: 2000-07-21
, NUMBER OF SEQ ID NOS: 19335
, SOFTWARE: Patent.pm
, SEQ ID NO 16454
, LENGTH: 203
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-621-976-16454

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[illegible]

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RESULT 4
US-09-621-976-16456
; Sequence 16456, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joberst, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTr and Encoded Human Proteins
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16456
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16456

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[illegible]

QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 5

US-09-621-976-16452
Sequence 16452, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16452
LENGTH: 355
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16452

Query Match 60.5%; Score 127.6; DB 4; Length 355;
Best Local Similarity 73.1%; Pred. No. 6.9e-37;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCCUGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60
QY 61 AUCGAUUGACUCCGAGUUGUCUGACCCUGCGAUUUUCCCAAUUGGGAACUCGACU 120
Db 61 ATCCATTGACCTCCGATGTGCTGACCCCTCGCATTTCCCAATGTGGGAACTCGACT 120
QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 6

US-09-497-855A-32
Sequence 32, Application US/09497855A
Patent No. 6605432
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGTH: 118067
TYPE: DNA
ORGANISM: Homo sapiens;
US-09-497-855A-32

Query Match 60.5%; Score 127.6; DB 4; Length 118067;
Best Local Similarity 73.1%; Pred. No. 9.7e-36;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCCUGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 59420 ATACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 59479

QY 61 AUCGAUUGACUCCGAGUUGUCUGACCCUGCGAUUUUCCCAAUUGGGAACUCGACU 120
Db 59480 ATCCATTGACCTCCGATGTGCTGACCCCTCGCATTTCCCAATGTGGGAACTCGACT 59539
QY 121 GCAGAAUUGGCCAU 134
Db 59540 GCATTAATTGTGTGT 59553

RESULT 7

US-09-621-976-16458
Sequence 16458, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16458
LENGTH: 204
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16458

Query Match 60.3%; Score 127.2; DB 4; Length 204;
Best Local Similarity 72.4%; Pred. No. 7.5e-37;
Matches 97; Conservative 33; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCCUGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60
QY 61 AUCGAUUGACUCCGAGUUGUCUGACCCUGCGAUUUUCCCAAUUGGGAACUCGACU 120
Db 61 ATCCATTGACCTCCGATGTGCTGACCCCTCGCATTTCCCAATGTGGGAACTCGACT 120
QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 8

US-09-621-976-16457
Sequence 16457, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16457
LENGTH: 189
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16457

Query Match 59.7%; Score 126; DB 4; Length 189;
Best Local Similarity 72.4%; Pred. No. 2e-36;
Matches 97; Conservative 32; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUAUCUACCCUGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60

[illegible]

Query Match:	55.4%	Score 116.8;	DB 1;	Length 164;
Best Local Similarity:	94.5%;	Pred. No. 4.3e-33;		
Matches 121;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	AUACUUAACUUGGAGGAGAGUACCAUGAUCAGAAAGUGUUUUCCAGGGCGAGGCU	60	
Db	1	AUACUUAACUUGGAGGAGAGUACCAUGAUCAGAAAGUGUUUUCCAGGGCGAGGCU	60	
QY	61	AUCCAUUGCAUCUCCGGAUUGUCUAGACCCUCGCAUUUCCCAAUUGUGGAAACUCGACU	120	
Db	61	AGCCAUUGCAUCUCCGGAUUGUCUAGACCCUCGCAUUUCCCAAUUGUGGAAACUCGACU	120	
QY	121	GCAGAAUUU	128	
Db	121	GCAGAAUUU	128	


```

FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 36424
LENGTH: 365
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 239
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 241
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 359
OTHER INFORMATION: x=a or g
US-09-513-999C-36424

Query Match          52.9%; Score 111.6; DB 4; Length 365;
Best Local Similarity 73.8%; Pred. No. 4.9e-31;
Matches 93; Conservative 24; Mismatches 9; Indels 0; Gaps 0

QY      9 CUGGACGGGGAGAUACCAUAGUACAAGAGUGGUUUCCAGGGCGAGCUUAUCGAUG 68
DB      127 CTGGCAGGGAGATACCATTCATGCAGAGGTGGTTTCCAGGGCGAGGCCATCATTG 68

QY      69 CACUCCGAGUGUGUGUGAACCCTCGGCAUUYCCCAAUUGUGGAAAUCGACUGAGAUAU 128
DB      67 CACTCCGGATGTGCGAACCCCTGCGACTCCCCCAAATGTGGAAACTGACTGATAATT 8

QY      129 GGCGAU 134
DB      7 TGTGT 2

RESULT 14
US-09-621-976-10271
Sequence 10271, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jodert, S.
TITLE OF INVENTION: Giordano, J.Y.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10271
LENGTH: 157
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-10271

Query Match          48.9%; Score 103.2; DB 4; Length 157;
Best Local Similarity 74.0%; Pred. No. 4e-28;
Matches 77; Conservative 27; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUCUACCGGCGAGGGAGAUACAUAUCAAGUAGUGUUUCCAGGGCGAGGCUU 60
DB      1 ATACTTACTGGCAGGGAGATASATGATCAAGAGTGGTTTTCCAGGGCGAGGCTT 60

QY      61 AUCCAUAUGCACUCCGGAUUGUCUACCCCGGCAUUYUCCCAAA 104
DB      61 ATCAATTGCACTCGGATGTGCTGACCCCTGCGATTTCCC AAA 104

```


QY	QY
12	12
121	121
181	181
181	181

RESULT 2

```

US-10-446-519-1
/ Sequence 1, Application US/10446519
/ Publication No. US20040006039A1
/ GENERAL INFORMATION:
/ APPLICANT: CHATTERJEE, SUBROTO B.
/ TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 58318-CIP (71699)
/ CURRENT APPLICATION NUMBER: US/10/446,519
/ CURRENT FILING DATE: 2003-05-27
/ PRIOR APPLICATION NUMBER: 10/279,215
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: 60/342,631
/ PRIOR FILING DATE: 2001-10-23
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 207
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-10-446-519-1

```

Query Match	73.0%;	Score 154;	DB 16;	Length 207;
Best Local Similarity	87.0%;	Pred. No. 1.2e-44;		
Matches 181; Conservative	0;	Mismatches 25;	Indels 2;	Gaps 1

QY	2	AUNCUAACCGGCAGAGGGAGAACCAUAGUCACGAAGUGGUTUUTCCAGGGCGAGGCTU	60
Db	1	AUNCUACCGGCAGAGGGAGAUACAUAUACGAAAGUGGUTUUTCCAGGGCGAGGCTU	60
QY	61	AUCCAUUGCACUCCGGGAUUGUCUGACCCCGCGAUUUTCCGAAUUGAGGGAAACUGACAU	120
Db	61	AUCCAUUGGCGUCCCGGAGUGUCUGACCCCGCGAUUUTCCGAAUUGAGGGAAACUCCACU	120
QY	121	GCGAAUUGGCGAUCUCCAGCACACTUGAUAUGUCCGUGAGACGAACGCGCCUCCGACGCAUUC	180
Db	121	GCAGAAUAUAGUACAUUAUUGCCUGAUGAGUCCGUGAGGACGAACCCUUCACAUAGAA	180
QY	181	UAGUGGGGGAUCUGCGUUCGCGCTUUTCCC	208
Db	181	AAGUGGGG--CUGCGUUCGCGCTUUTCCC	206

RESULT 3

```

US-10-446-519-2/c
/ Sequence 2, Application US/10446519
/ Publication No. US20040006039A1
/ GENERAL INFORMATION:
/ APPLICANT: CHATTERJEE, SUBROTO B.
/ TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 58318-CIP (71699)
/ CURRENT APPLICATION NUMBER: US/10/446,519
/ PRIOR FILING DATE: 2003-05-27
/ PRIOR APPLICATION NUMBER: 10/279,215
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: 60/442,631
/ PRIOR FILING DATE: 2001-10-23
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 207

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-519-2

```

Query Match	73.0%	Score 154;	DB 16;	Length 207;
Best Local Similarity	66.8%	Pred. NO. 1.2e-44;		
Matches 139; Conservative	42;	Mismatches 25;	Indels 2;	Gaps 1;

[illegible]

RESULT 4

US-10-276-302-3
Sequence 3, Application US/10276302
Publication No. US20030152967A1
GENERAL INFORMATION:
APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
APPLICANT: Murakami, Akinio
APPLICANT: Kojima, Kazuo
TITLE OF INVENTION: Methods and Kits for measuring antibodies against ENA
FILE REFERENCE: P021101
CURRENT APPLICATION NUMBER: US/10/276,302
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: JP P2000-157410
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 164
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Artificially
OTHER INFORMATION: synthesized primer sequence
US-10-276-302-3

Query Match	60.5%	Score 127.6;	DB 15;	Length 164;
Best Local Similarity	73.1%;	Pred. No. 3e-35;		
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

QY 1 AUAUUACUUGGCGAGGGAGAUUACCAUUAUCAGAAAGUGUUUUUCCGAGGGCGAGGUCU 60
Db 1 AATCTTACCTGGCAGGGAGATATCCATGATCATCCAAAGTGGTITTTCCGAGGGCAGGCTT 60
QY 61 AATCCATUAGCAGUCGGAGUUGUCUGACCCCTCCGCAUUTCCCAAAUUGUGGGAACUCGACU 120
Db 61 ATCCCATTTGACATCCCGAATGTGCTGACCCCTCCGATTTCCCAAAATGAGGAACCTGACT 120
QY 121 GCAGAAUUGGGCGAU 134
Db 121 GCATAATTGTGTGT 134

RESULT 5

US-10-027-632-286819/c
; Sequence 286819, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286819
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-286819
```

```
Query Match      60.5%; Score 127.6; DB 13; Length 553;
Best Local Similarity 73.1%; Pred. No. 3.9e-35;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 AUAUCUACUGGAGGAGAGAUACCAUGAUCAGAGUGUGUUUCCAGGCGAGGCUU 60
Db 444 ATACTTAACCTGGGAGGAGATACCATGATCAGAGGTGTTTCCAGGCGAGGCTT 385
Qy 61 AUCGAUUGGACUCCGAGUGUGUGACCCUGCGAUUUUCCCAAUUGUGGAAACUGGACU 120
Db 384 ATCCATTGACCTCCGATGTGCTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGACT 325
Qy 121 GCAGAAUUGGCGAU 134
Db 324 GCATAATTGTGTGT 311

RESULT 6
US-10-027-632-286819/c
; Sequence 286819, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286819
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-286819
```

```
Query Match      60.5%; Score 127.6; DB 15; Length 553;
Best Local Similarity 73.1%; Pred. No. 3.9e-35;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 AUAUCUACUGGAGGAGAGAUACCAUGAUCAGAGUGUGUUUCCAGGCGAGGCUU 60
Db 444 ATACTTAACCTGGGAGGAGATACCATGATCAGAGGTGTTTCCAGGCGAGGCTT 385
Qy 61 AUCGAUUGGACUCCGAGUGUGUGACCCUGCGAUUUUCCCAAUUGUGGAAACUGGACU 120
Db 384 ATCCATTGACCTCCGATGTGCTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGACT 325
Qy 121 GCAGAAUUGGCGAU 134
Db 324 GCATAATTGTGTGT 311
```

```
RESULT 7
US-10-081-327-32
; Sequence 32, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/10/081,327
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 06/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 06/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-10-081-327-32
```

```
Query Match      60.5%; Score 127.6; DB 15; Length 118067;
Best Local Similarity 73.1%; Pred. No. 1.3e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 AUAUCUACUGGAGGAGAGAUACCAUGAUCAGAGUGUGUUUCCAGGCGAGGCUU 60
Db 59420 ATACTTAACCTGGGAGGAGATACCATGATCAGAGGTGTTTCCAGGCGAGGCTT 59479
Qy 61 AUCGAUUGGACUCCGAGUGUGUGACCCUGCGAUUUUCCCAAUUGUGGAAACUGGACU 120
Db 59480 ATCCATTGACCTCCGATGTGCTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGACT 59539
Qy 121 GCAGAAUUGGCGAU 134
Db 59540 GCATAATTGTGTGT 59553
```

```
RESULT 8
US-10-029-386-18128
; Sequence 18128, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
```

```

US-10-029-386-4428

Query Match          57.4%; Score 121.2; DB 15; Length 515;
Best Local Similarity 70.9%; Pred. No. 7.5e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;

Qy      1  AUAUCUUAACCCUGGAGAGAUACCAUGAUAUCGAAAGGUGUUNUCCCGAGGCGGAGGU 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      267  ATACTTACTCTGGCAGTGGAGATACCATGATACGAAAGTGTTTCCAGGCGCGAGGCTT 326

Qy      61  AUCCAUUGCAUCUCCGGAUGUUGCCUGACCCCGUGCGAUNUUNCCCAUAUUGUGGAAACUCGACU 120
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      327  ATCCATCGACACTCCGGAATATGCTCAAGCCCTCGATTTTCCCAAAATGTGGAAACTCGACT 386

Qy      121  GCAGAUUGGCGAU 134
      |||:::|||||:::
Db      387  GCATTAATTTGTGT 400

RESULT 10
US-10-027-632-32256/c
; Sequence 32256, Application US/10027632
; Publication No. US20020196371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OR INVENTION: Identification and Mapping of Single Nucleotide

```

```

FILE REFERENCE: POLYMERPHISMS IN THE HUMAN GENOME
118827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ. ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 32256
LENGTH: 798
TYPE: DNA
ORGANISM: Human
US-10-027-632-32256

Query Match      57.4%   Score 121.2,   DB 13,   Length 798;
Best Local Similarity 70.9%   Pred. No. 8,2e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;

QY      1  AUAUUAACUUGAGGAGGGGAGAUUCCAUAGACAGAGAGUGUUUCCAGGCGAGGCTU 60
Db      206  ATCTTAACTCGGAGAGTGAGATATCCATGATCAGAGGTGTGTTTTCCAGGCGAGGCTT 147
QY      61  AUCCAUUGCAUCCCGGAGUGUGUGAGACCUCUGCAUUUCCCAAAUUGUGGAAACUAGCU 120
Db      146  ATCATATCGACATCTCGGATATAGCTGACCCCTGGCATTTTCCCAATGTGGAAACTCGACT 87
QY      121  GCAGAAUUGGCGAU 134
Db      86  GCATAATTGTGTGCT 73

RESULT 11
US-10-027-632-32256/c
Sequence 32256, Application US/10027632
Publication No. US20030204075A9

```

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FaSeq for windows Version 4.0
SEQ ID NO 32256
LENGTH: 798
TYPE: DNA
ORGANISM: Human
US-10-027-632-32256

Query Match 57.4%; Score 121.2; DB 15; Length 798;
Best Local Similarity 70.9%; Pred. No. 8.2e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;

QY 1 AUAUCUACCGGAGGAGAGUACCAUAGUACGAAAGUGGUGUUCGCCAGGCGAGGCUU 60
DB 206 ATACTTACCTGGGAGGAGATACATGATCAGAAAGTGTGTTCCAGGCGAGGCTT 147
DB 61 AUCGATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 87
QY 146 ATCATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 87
QY 121 GCAGAUUGGCGAU 134
DB 86 GCATATTTGTGTGT 73

RESULT 12
US-10-775-169-82
Sequence 82, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dornier, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 82
LENGTH: 127917
TYPE: DNA
ORGANISM: Homo sapiens
US-10-775-169-82

Query Match 57.4%; Score 121.2; DB 17; Length 127917;
Best Local Similarity 70.9%; Pred. No. 2.5e-32;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;
QY 1 AUAUCUACCGGAGGAGAGUACCAUAGUACGAAAGUGGUGUUCGCCAGGCGAGGCUU 60

DB 36936 ATACTTACCTGGGAGGAGATACATGATCAGAAAGTGTGTTCCAGGCGAGGCTT 36995
QY 61 AUCGATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 120
DB 36996 ATCATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 37055
QY 121 GCAGAUUGGCGAU 134
DB 37056 GCATATTTGTGTGT 37069

RESULT 13
US-10-027-632-79716/C
Sequence 79716, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FaSeq for windows Version 4.0
SEQ ID NO 79716
LENGTH: 539
TYPE: DNA
ORGANISM: Human
US-10-027-632-79716

Query Match 54.2%; Score 114.4; DB 13; Length 539;
Best Local Similarity 66.4%; Pred. No. 2e-30;
Matches 89; Conservative 33; Mismatches 12; Indels 0; Gaps 0;

QY 1 AUAUCUACCGGAGGAGAGUACCAUAGUACGAAAGUGGUGUUCGCCAGGCGAGGCUU 60
DB 359 ATACTTACCTGGGAGGAGATACATGATCAGAAAGTGTGTTCCAGGCGAGGCTT 300
QY 61 AUCGATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 120
DB 299 ATCATGCGACCTCGGATGATGACCCCTGCGATTTCCCAATGTGGAACTCGACT 240
QY 121 GCAGAUUGGCGAU 134
DB 239 GCATATTTGTGTGT 226

RESULT 14
US-10-027-632-314864/C
Sequence 314864, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

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; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314864
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314864
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Query Match          54.2%; Score 114.4; DB 13; Length 539;
Best Local Similarity 66.4%; Pred. No. 2e-30;
Matches 89; Conservative 33; Mismatches 12; Indels 0; Gaps 0;
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Qy      1 AUAUCUACCCUGCAGAGGAGAUACCAUGAUCCAGAGUGUUUCCAGGCGAGGCUU 60
      359 ATACTTAGCTGCGAGAGAAATACCATGATCACAAGGTGGTTTCCAGGGTGAGGTTT 300
Qy      61 AUCGAUUGCACCUGGAGUGUCUGACCCUUGCGAUUUCCCAAUUGUGGAAACUCGACU 120
      299 ATCCATTAACTCAGAGATGCTGACCCCTGCRATTTCCCAATGTGGAACTCACT 240
Db      121 GCAGAAUUGCGCAU 134
      239 GCATTAATTGGTAT 226
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RESULT 15
US-10-027-632-79716/c
; Sequence 79716, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79716
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-79716
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Query Match          54.2%; Score 114.4; DB 15; Length 539;
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```

Best Local Similarity 66.4%; Pred. No. 2e-30;
Matches 89; Conservative 33; Mismatches 12; Indels 0; Gaps 0;
Qy      1 AUAUCUACCCUGCAGAGGAGAUACCAUGAUCCAGAGUGUUUCCAGGCGAGGCUU 60
      359 ATACTTAGCTGCGAGAGAAATACCATGATCACAAGGTGGTTTCCAGGGTGAGGTTT 300
Db      61 AUCGAUUGCACCUGGAGUGUCUGACCCUUGCGAUUUCCCAAUUGUGGAAACUCGACU 120
      299 ATCCATTAACTCAGAGATGCTGACCCCTGCRATTTCCCAATGTGGAACTCACT 240
Qy      121 GCAGAAUUGCGCAU 134
      239 GCATTAATTGGTAT 226
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Search completed: January 19, 2005, 23:36:58
Job time : 304 secs
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QY      61 AUCCAUUGGACUCCGGAUGUGUGACCCGCGAUAUUCGCCAAUUGUGGAAAUCUGACU 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      231 ATCCATTGCACTCCGGAATGTGCTACCCCTCGATTTCCTCAATGTGGAACTCGACT 172
QY      121 GCAGAUUGGCGAU 134
      |||:|||||:
Db      171 GCATTAATTTGTGCT 158

RESULT 2
LOCUS   AL705609                468 bp    mRNA    linear    EST 04-SEP-2003
DEFINITION DKFZP686L2236.r1.666 (synonym: h1cc3) Homo sapiens cDNA clone
ACCESSION AL705609
VERSION   AL705609
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 468)
AUTHORS   Wamburt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
TITLE     EST (Wamburt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
MIPS      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZP686L2236) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
LOCATION/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686L2236"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="686 (synonym: h1cc3)"
/notes="Vector: pTriplEx2; Site_1: SfiIA, Site_2: SfiIB,
cDNA-collection"

FEATURES
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1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686L2236"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="686 (synonym: h1cc3)"
/notes="Vector: pTriplEx2; Site_1: SfiIA, Site_2: SfiIB,
cDNA-collection"

ORIGIN
Query Match      60.5%; Score 127.6; DB 1; Length 468;
Best Local Similarity 73.1%; Pred. No. 1.5e-29;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY      1 AUACUUAACCTGGCAGAGGAGAUACCAUGACGAAAGUGUUUCCAGAGGCGAGGCU 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      223 ATACTTAACCTGGCAGAGGAGATACCATGATCAGGAAGTGTGTTTCCAGAGGCGAGGCTT 282
QY      61 AUCCAUUGGACUCCGGAUGUGUGACCCGCGAUAUUCGCCAAUUGUGGAAAUCUGACU 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      283 ATCCATTGCACTCCGGAATGTGCTACCCCTCGATTTCCTCAATGTGGAACTCGACT 342
QY      121 GCAGAUUGGCGAU 134
      |||:|||||:
Db      343 GCATTAATTTGTGCT 356

RESULT 3
LOCUS   BM749651                556 bp    mRNA    linear    EST 04-MAR-2002
DEFINITION K-EST0024911 S11SNUI Homo sapiens cDNA clone S11SNUI-4-H10 5', mRNA
sequence.
ACCESSION BM749651

```

```

VERSION   BM749651.1 GI:190792269
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 556)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.U., Cheong,U.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: H column: 10
High quality sequence scop: 556.
LOCATION/Qualifiers
1..556
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S11SNUI-4-H10"
/sex="M"
/cissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SN-1"
/lab_host="Top10F"
/clone.lib="S11SNUI"
/notes="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
Site_2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII- digested pME18S-Pf3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match      60.5%; Score 127.6; DB 4; Length 556;
Best Local Similarity 73.1%; Pred. No. 1.5e-29;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY      1 AUACUUAACCTGGCAGAGGAGAUACCAUGACGAAAGUGUUUCCAGAGGCGAGGCU 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      12 ATACTTAACCTGGCAGAGGAGATACCATGATCAGGAAGTGTGTTTCCAGAGGCGAGGCTT 71
QY      61 AUCCAUUGGACUCCGGAUGUGUGACCCGCGAUAUUCGCCAAUUGUGGAAAUCUGACU 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      72 ATCCATTGCACTCCGGAATGTGCTACCCCTCGATTTCCTCAATGTGGAACTCGACT 131
QY      121 GCAGAUUGGCGAU 134
      |||:|||||:
Db      132 GCATTAATTTGTGCT 145

RESULT 4
LOCUS   BP455568                565 bp    mRNA    linear    EST 31-DEC-2003
DEFINITION BP455568 full-length enriched swine cDNA library, adult ovary Sus
scrofa cDNA clone OVRM10152B01 5', mRNA sequence.
ACCESSION BP455568

```

JOURNAL
 COMMENT
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 4 row: E column: 11
 High quality sequence stop: 567.
 Location/Qualifiers
 1..567
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="U13SNJ387-4-E11"
 /sex="F"
 /tissue_type="liver"
 /cell_type="Epithelial"
 /cell_line="SNU-387"
 /lab_host="T0p10F"
 /clone_1ib="U13SNJ387"
 /note="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then deapped
 with tabacco acid pyrophosphatase (TAP). The deapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli T0p10F by electroporation method
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN
 Query Match 60.5%; Score 127.6; DB 6; Length 567;
 Best Local Similarity 73.1%; Pred. No. 1.5e-29;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 AUACUUAACUUGGAGGAGGAGUACCAUGAUGAAGUGUUNUCCAGAGCGGAGGU 60
 Db 1 ATACTTACCTGGCGAGGGAGATACCAATGATACAGAGGTGGTTTCCAGAGCGGCTT 60
 Oy 61 AUCCAUUGCAUCUCGGAUGUGUCUGACCCGUCGAGUUNUCCCAUAUNUGUGGAAACUCGACU 120
 Db 61 ATCATTTGCACTCCGGAGATGTCGTACCCCTGTCGATTTCCCAAAATGTCGAAATCGACT 120
 Oy 121 GCAGAUUGGCGAU 134
 Db 121 GCATATATTGTGT 134

RESULT 6
 BP452975
 LOCUS
 DEFINITION
 BP452975 full-length enriched swine cDNA library, adult liver Sus
 BP452975
 ACCESSION
 VERSION
 KEYWORDS
 BP452975.1 GI:40443042
 EST.
 Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 1 (bases 1 to 602)
 Udenishi, H., Egnuchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
 Okumura, N., Hamasina, N. and Awata, T.
 PEDF (Pig EST Data Explorer): construction of a database for ESTs

QY 1 AUAUUUACCCGAGGAGGAGAUACCAUGAUCAGAAAGUGUUUCCAGAGGAGGAGCU 60
 Db 1 ATACTTACCTGGAGGAGGAGATACATGATCAGAAAGTGTTTCCAGAGGAGGCTT 60
 QY 61 AUCCAUUGCAGUCUCCGAGUAGUGUGUACCCUGCGAUUUUCCCAAUUGUGGAAACUCGACU 120
 Db 61 ATCCATTGACCTCCGATGTGTGACCCCTCGCATTTCCCAATGTGGGAAACTCGACT 120
 QY 121 GCAGAAUUGGCGCAU 134
 Db 121 GCATAATTGTGTGT 134

RESULT 9
 CE201300/c 715 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000372228685 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE201300
 VERSION CE201300.1 GI:35356955
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 715)
 Kirhnes,E.F., Balne,V., Halpern,A.L., Levy,S., Remington,K.,
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 14512627
 CONTACT: Kirhnes EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirhnes@tigr.org
 Class: shotgun.

FEATURES
 source Location/Qualifiers
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 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BACXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 60.5%; Score 127.6; DB 9; Length 715;
 Best Local Similarity 73.1%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
 Matches 98; Conservative 32; Mismatches 4;

QY 1 AUAUUUACCCGAGGAGGAGAUACCAUGAUCAGAAAGUGUUUCCAGAGGAGGAGCU 60
 Db 329 ATACTTACCTGGAGGAGGAGATACATGATCAGAAAGTGTTTCCAGAGGAGGCTT 270
 QY 61 AUCCAUUGCAGUCUCCGAGUAGUGUGUACCCUGCGAUUUUCCCAAUUGUGGAAACUCGACU 120
 Db 269 ATCCATTGACCTCCGATGTGTGACCCCTCGCATTTCCCAATGTGGGAAACTCGACT 210
 QY 121 GCAGAAUUGGCGCAU 134
 Db 209 GCATAATTGTGTGT 196

RESULT 10
 BP147290 742 bp mRNA linear EST 30-DEC-2003
 LOCUS BP147290

DEFINITION BP147290 full-length enriched swine cDNA library, adult ovary Sus
 scrofa cDNA clone OVRM10127B1.5', mRNA sequence.
 ACCESSION BP147290
 VERSION BP147290.1 GI:40396761
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 742)
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamasima,N. and Awata,T.
 PEDS (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 Contact: Hirohide Uenishi
 National Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.

FEATURES
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 1..742
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="OVRM10127B1.1"
 /issue_type="ovary"
 /dev_stage="adult"
 /clone_lib="Full-length enriched swine cDNA library, adult
 ovary"

ORIGIN
 Query Match 60.5%; Score 127.6; DB 5; Length 742;
 Best Local Similarity 73.1%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
 Matches 98; Conservative 32; Mismatches 4;

QY 1 AUAUUUACCCGAGGAGGAGAUACCAUGAUCAGAAAGUGUUUCCAGAGGAGGAGCU 60
 Db 1 ATACTTACCTGGAGGAGGAGATACATGATCAGAAAGTGTTTCCAGAGGAGGCTT 60
 QY 61 AUCCAUUGCAGUCUCCGAGUAGUGUGUACCCUGCGAUUUUCCCAAUUGUGGAAACUCGACU 120
 Db 61 ATCCATTGACCTCCGATGTGTGACCCCTCGCATTTCCCAATGTGGGAAACTCGACT 120
 QY 121 GCAGAAUUGGCGCAU 134
 Db 121 GCATAATTGTGTGT 134

RESULT 11
 BP437373 781 bp mRNA linear EST 30-DEC-2003
 LOCUS BP437373
 DEFINITION BP437373 full-length enriched swine cDNA library, adult lung Sus
 scrofa cDNA clone LING010036B06.5', mRNA sequence.
 ACCESSION BP437373
 VERSION BP437373.1 GI:40427440
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 781)
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,

Okumura, N., Hamashima, N. and Awata, T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uemishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agricultural Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="txacon:9823"
/clone="LNG01.10036026"
/tissue_type="lung"
/dev_stage="adult"
/clone_1b="full-length enriched swine cDNA library, adult
lung"

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Query Match	60.5%;	Score 127.6;	DB 5;	Length 781;
Best Local Similarity	73.1%;	Pred. No. 1.6e-29;		
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	AUUCVUAACUGGAGCGGGAGAUUCCAUUAUUCACGAAGUGUUUUCCAGGGCCAGGCTU	60
Db	1	ATACTTACTCCTGGAGGGGAGATACCATCATGATCACGAAGTGTTTCCAGGCGGAGGCTT	60
QY	61	AUCCAUUUGCAUCCGGGANUGGCUAACCUCUCCGANTUCCCCAAANUGUGGAAAUCUGACU	120
Db	61	ATCCATTTCGCATCCGGGATGTCTGACCCCTCGATTTCGCCAAATGTGGGAAACTGACT	120
QY	121	GCGAGAUUGGCGAU	134
Db	121	GCATTAATTGTGGT	134

RESULT 12	CC491649/c	LOCUS	CC491649	796 bp	DNA	linear	GSS 17-JUN-2003
DEFINITION	CH240_325G6, TARBAC13P2 CHORI-240 Bos taurus genomic clone						
DEFINITION	CH240_325G6, genomic survey sequence.						
CC491649							
CC491649							

TITLE	Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
JOURNAL	Unpublished (2003)
COMMENT	Other_GSSs: CH240_325G6.T7

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/clone lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI, Site 2: MboI
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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Query Match	60.5%;	Score 127.6;	DB 9;	Length 796;
Best Local Similarity	73.1%;	Pred. No. 1.6e-29;		
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

RESULT 13	LOCUS	DEFINITION
BP144031	809 bp	mRNA
BP144031	full-length enriched swine cDNA library, adult ovary	EST 30-DEC-2003
scfafa cDNA clone OVR010018G03 5', mRNA sequence.		

JOURNAL
COMMENT

National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishh@affrc.go.jp

QY	61	AUCCAUUGCACTCCGGAGUUGUGACCCUUGCGAUUUCCCCAAUUGUGGAAACUUGACU	120
Db	61	ATCCATTGCACTCCGGATGTGTGACCCCTCGATTTCGCCAATGTGGGAACTCAGCT	120
QY	121	GCAGAAUUGGCGAU	134
Db	121	GCATAATTGTGTGT	134

Search completed: January 19, 2005, 18:18:15
 Job time : 1842 secs